

ABSTRACT

5 The present invention presents methods for gene expression monitoring that utilize
microelectronic arrays to drive the transport and hybridization of nucleic acids.
Procedures are described for generating mRNA expression samples for use in these
methods from populations of cells, tissues, or other biological source materials, that may
differ in their physiological and/or pathological state. Provided in the invention are
methods for generating a reusable nucleic acid transcript library from mRNA in a sample
10 of biological material. In order to improve gene expression monitoring on the
microelectronic arrays, the transcripts are amplified to produce sample nucleic acid
amplicons of a defined length. Because multiple sample amplicons may be selectively
hybridized to controlled sites in the electronic array, the gene expression profiles of the
polynucleotide populations from different sources can be directly compared in an array
15 format using electronic hybridization methodologies. Also provided in the invention are
methods for detecting the level of sample amplicons using electronically assisted primer
extension detection, and utilizing individual test site hybridization controls. The
hybridization data collected utilizing the improved methods of the present invention will
allow the correlation of changes in mRNA level with the corresponding expression of the
20 encoded protein in the biological source material, and thus aid in studying the role of gene
expression in disease.